CLAIMS

1. A method for estimating the risk for development of carcinoma in a human being exposed to human papilloma virus(es) (HPV), comprising
(i) identification of one or more of said HPV or groups thereof in a sample from said human being;
(ii) calculating the amount of HPV of each type or group in the sample and normalising the values to the amount of cells sampled;
(iii) estimating the risk for each of the HPV or groups of HPV by comparing each viral titer value from (ii) with type or group specific standard curves for each viral type or group with risk estimation values; and
(iv) estimating the combined risk for carcinoma development for the human being from the individual risk estimation curves of the different viral types.

2. A method according to claim 1, wherein the amount of HPV is determined by amplification.

3. A method according to claims 1 or 2, wherein the HPV is selected from HPV 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 67 and 68.

4. A method according to claims 1 or 2, wherein the HPV is selected from HPV 16, 18, 31, 33, 35, 39, 45, 52 and 58.

5. A method according to one or more of the claims 1-4, wherein the risk estimation values may be odds ratio (OR), relative risk (RR) and/or positive predictive values (PPV).

6. A method according to one or more of the claims 1-5, wherein the human being is a woman and the carcinoma is cervical carcinoma in situ (CIS).

7. A method according to claim 6, wherein optionally the age of the woman is taken into account in steps (iii) and/or (iv).